



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/019,963

DATE: 01/24/2002
TIME: 12:32:08

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3 <110> APPLICANT: Aventis Research & Technologies GmbH & Co KG
5 <120> TITLE OF INVENTION: Novel Antifungal Agents and Fungicides, Method for the
Production

6 Thereof and Their Use

8 <130> FILE REFERENCE: 199at07

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/019,963

C--> 11 <141> CURRENT FILING DATE: 2002-01-03

13 <150> PRIOR APPLICATION NUMBER: DE19930959.0

14 <151> PRIOR FILING DATE: 1999-07-05

16 <160> NUMBER OF SEQ ID NOS: 4

18 <170> SOFTWARE: PatentIn Ver. 2.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 930

22 <212> TYPE: DNA

23 <213> ORGANISM: Williopsis californica

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (1)..(930)

29 <400> SEQUENCE: 1

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31	Met	Arg	Phe	Thr	Thr	Leu	Val	Ala	Leu	Ala	Gly	Ala	Ile	Ser	Ser	Val	
32	1				5				10					15			
34	cag	gcc	atc	ggc	caa	cta	gct	ttt	aac	ttg	ggt	gtc	aag	gat	aac	tca	96
35	Gln	Ala	Ile	Gly	Gln	Leu	Ala	Phe	Asn	Leu	Gly	Val	Lys	Asp	Asn	Ser	
36				20				25					30				
38	ggt	cag	tgc	aag	act	gcc	tca	gag	tac	aag	gat	gac	ttg	tct	acc	ctt	144
39	Gly	Gln	Cys	Lys	Thr	Ala	Ser	Glu	Tyr	Lys	Asp	Asp	Leu	Ser	Thr	Leu	
40				35				40					45				
42	tca	ggc	tac	aca	tct	aag	gtt	aga	gtc	tac	gct	gcc	tca	gac	tgt	aac	192
43	Ser	Gly	Tyr	Thr	Ser	Lys	Val	Arg	Val	Tyr	Ala	Ala	Ser	Asp	Cys	Asn	
44		50				55				60							
46	act	ttg	cag	act	ttg	ggt	cca	gtt	gtc	gaa	gag	gct	ggc	ttc	tca	ttt	240
47	Thr	Leu	Gln	Thr	Leu	Gly	Pro	Val	Val	Glu	Ala	Gly	Phe	Ser	Phe		
48	65				70					75				80			
50	ttc	gtt	ggt	att	tgg	cca	aac	gat	gat	gct	cac	ttc	cag	gaa	gag	caa	288
51	Phe	Val	Gly	Ile	Trp	Pro	Asn	Asp	Asp	Ala	His	Phe	Gln	Glu	Glu	Gln	
52				85				90					95				
54	gac	gct	ttg	aaa	act	tat	ttg	cca	aag	att	aag	aga	tcc	aca	gtg	gag	336
55	Asp	Ala	Leu	Lys	Thr	Tyr	Leu	Pro	Lys	Ile	Lys	Arg	Ser	Thr	Val	Glu	
56				100				105					110				
58	gcc	ttc	act	gtt	ggt	tct	gag	gcc	ttg	tat	aga	gat	gat	atg	act	gct	384
59	Ala	Phe	Thr	Val	Gly	Ser	Glu	Ala	Leu	Tyr	Arg	Asp	Asp	Met	Thr	Ala	
60				115				120					125				
62	caa	gag	ttg	gct	gac	aga	atc	aaa	act	att	aga	gag	ttg	gtt	gcc	act	432

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67 Ile Asp Asp Ser Glu Gly Asn Ser Tyr Ala Gly Ile Pro Val Gly Phe
68 145                      150                      155                      160
70 gtt gac tcc tgg aac gtt ttg gtt gat ggt gct tct cac cca gct att 528
71 Val Asp Ser Trp Asn Val Leu Val Asp Gly Ala Ser His Pro Ala Ile
72                      165                      170                      175
74 gtt gag gct gat gtt gtg ttc gcc aat gct ttc tct tac tgg caa ggt 576
75 Val Glu Ala Asp Val Val Phe Ala Asn Ala Phe Ser Tyr Trp Gln Gly
76                      180                      185                      190
78 cag act cag cag aac tcg tca tac tct ttc ttt gac gac att atg caa 624
79 Gln Thr Gln Gln Asn Ser Ser Tyr Ser Phe Phe Asp Asp Ile Met Gln
80                      195                      200                      205
82 gct ttg caa acc att caa act gct aag ggt gag aca gat atc act ttc 672
83 Ala Leu Gln Thr Ile Gln Thr Ala Lys Gly Glu Thr Asp Ile Thr Phe
84                      210                      215                      220
86 tgg gtt ggt gag acc ggc tgg cca acc gat ggt act cac ttt gaa gac 720
87 Trp Val Gly Glu Thr Gly Trp Pro Thr Asp Gly Thr His Phe Glu Asp
88 225                      230                      235                      240
90 tct gtc cca tct gtt gag aat gct cag acc ttc tgg aaa gat gcc gtc 768
91 Ser Val Pro Ser Val Glu Asn Ala Gln Thr Phe Trp Lys Asp Ala Val
92                      245                      250                      255
94 tgt gcc att aga ggt tgg ggt atc aat gtt att gcc ttt gag gcc ttt 816
95 Cys Ala Ile Arg Gly Trp Gly Ile Asn Val Ile Ala Phe Glu Ala Phe
96                      260                      265                      270
98 gac gaa gct tgg aag cca gat acc tct ggt acc tct gat gtg gaa aag 864
99 Asp Glu Ala Trp Lys Pro Asp Thr Ser Gly Thr Ser Asp Val Glu Lys
100                      275                      280                      285
102 tac tgg ggt gtt tgg gac tct aac agc aag ttg aag tat gat ttg tcc 912
103 Tyr Trp Gly Val Trp Asp Ser Asn Ser Lys Leu Lys Tyr Asp Leu Ser
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107 Cys Asp Phe Thr Ser
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120 20 25 30
121 Gly Gln Cys Lys Thr Ala Ser Glu Tyr Lys Asp Asp Leu Ser Thr Leu
122 35 40 45
123 Ser Gly Tyr Thr Ser Lys Val Arg Val Tyr Ala Ala Ser Asp Cys Asn
124 50 55 60
125 Thr Leu Gln Thr Leu Gly Pro Val Val Glu Glu Ala Gly Phe Ser Phe

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126 65          70          75          80
127 Phe Val Gly Ile Trp Pro Asn Asp Asp Ala His Phe Gln Glu Glu Gln
128          85          90          95
129 Asp Ala Leu Lys Thr Tyr Leu Pro Lys Ile Lys Arg Ser Thr Val Glu
130          100          105          110
131 Ala Phe Thr Val Gly Ser Glu Ala Leu Tyr Arg Asp Asp Met Thr Ala
132          115          120          125
133 Gln Glu Leu Ala Asp Arg Ile Lys Thr Ile Arg Glu Leu Val Ala Thr
134          130          135          140
135 Ile Asp Asp Ser Glu Gly Asn Ser Tyr Ala Gly Ile Pro Val Gly Phe
136 145          150          155          160
137 Val Asp Ser Trp Asn Val Leu Val Asp Gly Ala Ser His Pro Ala Ile
138          165          170          175
139 Val Glu Ala Asp Val Val Phe Ala Asn Ala Phe Ser Tyr Trp Gln Gly
140          180          185          190
141 Gln Thr Gln Gln Asn Ser Ser Tyr Ser Phe Phe Asp Asp Ile Met Gln
142          195          200          205
143 Ala Leu Gln Thr Ile Gln Thr Ala Lys Gly Glu Thr Asp Ile Thr Phe
144          210          215          220
145 Trp Val Gly Glu Thr Gly Trp Pro Thr Asp Gly Thr His Phe Glu Asp
146 225          230          235          240
147 Ser Val Pro Ser Val Glu Asn Ala Gln Thr Phe Trp Lys Asp Ala Val
148          245          250          255
149 Cys Ala Ile Arg Gly Trp Gly Ile Asn Val Ile Ala Phe Glu Ala Phe
150          260          265          270
151 Asp Glu Ala Trp Lys Pro Asp Thr Ser Gly Thr Ser Asp Val Glu Lys
152          275          280          285
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154          290          295          300
155 Cys Asp Phe Thr Ser
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161 <211> LENGTH: 717
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163 <213> ORGANISM: Zygosaccharomyces bailii
165 <220> FEATURE:
166 <221> NAME/KEY: CDS
167 <222> LOCATION: (1)..(717)
169 <400> SEQUENCE: 3
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172 1 5 10 15
174 ata tat act agt gct aga aac ata tta gac aga gaa tac aca gca aac 96
175 Ile Tyr Thr Ser Ala Arg Asn Ile Leu Asp Arg Glu Tyr Thr Ala Asn
176 20 25 30
178 gaa tta aaa act gct ttt gga gat gaa gaa att ttt aca gat ttg acg 144
179 Glu Leu Lys Thr Ala Phe Gly Asp Glu Glu Ile Phe Thr Asp Leu Thr
180 35 40 45
182 tat cac att cac gtt aac gtc agt ggc gaa att gac tct tac tat cat 192

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183 Tyr His Ile His Val Asn Val Ser Gly Glu Ile Asp Ser Tyr Tyr His
184      50                      55                      60
186 aat tta gtc aat ttt gtc gat aac gct cta gca aac aaa gat att aat 240
187 Asn Leu Val Asn Phe Val Asp Asn Ala Leu Ala Asn Lys Asp Ile Asn
188 65                      70                      75                      80
190 aga tat ata tac gct ata ttt aca cag cag aca aac tat aca gag gat 288
191 Arg Tyr Ile Tyr Ala Ile Phe Thr Gln Gln Thr Asn Tyr Thr Glu Asp
192                      85                      90                      95
194 ggg ctc att gag tac tta aat cat tac gat tca gag act tgc aaa gat 336
195 Gly Leu Ile Glu Tyr Leu Asn His Tyr Asp Ser Glu Thr Cys Lys Asp
196                      100                      105                      110
198 atc att act cag tat aat gtt aac gta gac act agt aac tgt ata agc 384
199 Ile Ile Thr Gln Tyr Asn Val Asn Val Asp Thr Ser Asn Cys Ile Ser
200                      115                      120                      125
202 aat act aca gat caa gct aga ctc caa cgt cgc gga ggg tgg gtg aac 432
203 Asn Thr Thr Asp Gln Ala Arg Leu Gln Arg Arg Gly Gly Trp Val Asn
204                      130                      135                      140
206 cca cat tgt agt ggt gat aac tta gcc gat act agc gat tgt tgt aac 480
207 Pro His Cys Ser Gly Asp Asn Leu Ala Asp Thr Ser Asp Cys Cys Asn
208 145                      150                      155                      160
210 ttg gct tat aac aag att aac ccc tct tca aac tta cag tca tgg aat 528
211 Leu Ala Tyr Asn Lys Ile Asn Pro Ser Ser Asn Leu Gln Ser Trp Asn
212                      165                      170                      175
214 tat gtt gtc ggg cag tgt cac tat att tct cac gct aat gga aag gta 576
215 Tyr Val Val Gly Gln Cys His Tyr Ile Ser His Ala Asn Gly Lys Val
216                      180                      185                      190
218 tgt agt ggt gct gac agg caa cag tta gct gaa aat gta tgt aac tgg 624
219 Cys Ser Gly Ala Asp Arg Gln Gln Leu Ala Glu Asn Val Cys Asn Trp
220                      195                      200                      205
222 tgt cag gtt aac ggt ggt gtt agc gct ttt gct agc agt agt tct gca 672
223 Cys Gln Val Asn Gly Gly Val Ser Ala Phe Ala Ser Ser Ser Ser Ala
224                      210                      215                      220
226 cat cca ggt gct tgc atg agt gat gta ggg ttc tgc tat gct tag 717
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228 225                      230                      235
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232 <211> LENGTH: 238
233 <212> TYPE: PRT
234 <213> ORGANISM: Zygosaccharomyces bailii
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239 Ile Tyr Thr Ser Ala Arg Asn Ile Leu Asp Arg Glu Tyr Thr Ala Asn
240                      20                      25                      30
241 Glu Leu Lys Thr Ala Phe Gly Asp Glu Glu Ile Phe Thr Asp Leu Thr
242                      35                      40                      45
243 Tyr His Ile His Val Asn Val Ser Gly Glu Ile Asp Ser Tyr Tyr His
244 50                      55                      60
245 Asn Leu Val Asn Phe Val Asp Asn Ala Leu Ala Asn Lys Asp Ile Asn

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247	Arg	Tyr	Ile	Tyr	Ala	Ile	Phe	Thr	Gln	Gln	Thr	Asn	Tyr	Thr	Glu	Asp
248					85				90						95	
249	Gly	Leu	Ile	Glu	Tyr	Leu	Asn	His	Tyr	Asp	Ser	Glu	Thr	Cys	Lys	Asp
250					100				105						110	
251	Ile	Ile	Thr	Gln	Tyr	Asn	Val	Asn	Val	Asp	Thr	Ser	Asn	Cys	Ile	Ser
252					115				120						125	
253	Asn	Thr	Thr	Asp	Gln	Ala	Arg	Leu	Gln	Arg	Arg	Gly	Gly	Trp	Val	Asn
254					130				135						140	
255	Pro	His	Cys	Ser	Gly	Asp	Asn	Leu	Ala	Asp	Thr	Ser	Asp	Cys	Cys	Asn
256	145					150					155					160
257	Leu	Ala	Tyr	Asn	Lys	Ile	Asn	Pro	Ser	Ser	Asn	Leu	Gln	Ser	Trp	Asn
258					165					170						175
259	Tyr	Val	Val	Gly	Gln	Cys	His	Tyr	Ile	Ser	His	Ala	Asn	Gly	Lys	Val
260					180					185					190	
261	Cys	Ser	Gly	Ala	Asp	Arg	Gln	Gln	Leu	Ala	Glu	Asn	Val	Cys	Asn	Trp
262					195				200					205		
263	Cys	Gln	Val	Asn	Gly	Gly	Val	Ser	Ala	Phe	Ala	Ser	Ser	Ser	Ser	Ala
264					210				215					220		
265	His	Pro	Gly	Ala	Cys	Met	Ser	Asp	Val	Gly	Phe	Cys	Tyr	Ala		
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/019,963

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1